

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 22:41:32 ; Search time 391 Seconds  
(without alignments)  
9952.565 Million cell updates/sec

Title: US-09-847-081B-1  
Perfect score: 1728  
Sequence: 1 agaaacccagaagaacac.....tcatcaaacctcaagtga 1728

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 1728  | 100.0       | 1728   | AAI66366 | Nicotiana tabacum  |
| 2          | 868   | 50.2        | 1826   | AAV03880 | Phytoene synthase  |
| 3          | 858.6 | 49.7        | 1795   | AAV03878 | Phytoene synthase  |
| 4          | 857.8 | 49.6        | 1712   | AAI66367 | Nicotiana tabacum  |
| 5          | 853.4 | 49.4        | 1814   | AAV03881 | Phytoene synthase  |
| 6          | 847.6 | 49.1        | 1591   | AAQ99323 | Melon phytoene-syn |
| 7          | 840.4 | 48.6        | 1646   | AAQ12495 | Tomato fruit ripen |
| 8          | 811.2 | 46.9        | 1316   | AAV03879 | Phytoene synthase  |
| 9          | 806.4 | 46.7        | 1239   | AAZ99482 | CDNA encoding a ph |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    |       |      |         |    |           |                     |
|----|-------|------|---------|----|-----------|---------------------|
| 10 | 692.4 | 40.1 | 2868    | 19 | AAV16951  | Nucleic acid encod  |
| 11 | 678.4 | 39.3 | 1921    | 19 | AAV16949  | Nucleic acid encod  |
| 12 | 670.4 | 38.8 | 2085    | 19 | AAV16948  | Nucleic acid encod  |
| 13 | 653.4 | 37.8 | 1932    | 19 | AAV16950  | Nucleic acid encod  |
| 14 | 578.6 | 33.5 | 1703    | 21 | AAAC35120 | Arabidopsis thalia  |
| 15 | 578.4 | 33.5 | 1566    | 21 | AAAC4162  | Arabidopsis thalia  |
| 16 | 548.2 | 31.7 | 1397    | 21 | AAZ29145  | Soybean phytoene s  |
| 17 | 512.2 | 29.6 | 1304    | 24 | ABA97361  | Nucleotide sequenc  |
| 18 | 456.8 | 26.4 | 992     | 21 | AAZ29144  | Soybean phytoene s  |
| 19 | 424   | 24.5 | 1448    | 21 | AAZ29139  | Corn phytoene synt  |
| 20 | 415.2 | 24.0 | 1239    | 19 | AAV17247  | Wheat phytoene synt |
| 21 | 401   | 23.2 | 1021    | 21 | AAZ29146  | Rice phytoene synt  |
| 22 | 388.8 | 22.5 | 1060    | 21 | AAZ29143  | psy A encoding seq  |
| 23 | 290.6 | 16.8 | 2585    | 23 | ABL41600  | Corn phytoene synt  |
| 24 | 251.4 | 14.5 | 888     | 21 | AAZ29140  | Fragment of GROM5   |
| 25 | 223.8 | 13.0 | 3485    | 13 | AAQ29121  | Physcomitrella pat  |
| 26 | 177.4 | 10.3 | 584     | 22 | AAH44248  | Phytoene synthase   |
| 27 | 172   | 10.0 | 749     | 19 | AAV03882  | Rice phytoene synt  |
| 28 | 170.2 | 9.8  | 476     | 21 | AAZ29142  | Fragment contg. pr  |
| 29 | 145.6 | 8.4  | 1386    | 13 | AAQ29122  | Rice phytoene synt  |
| 30 | 121.8 | 7.0  | 766     | 21 | AAZ29141  | N. meningitidis pa  |
| 31 | 59.2  | 3.4  | 56609   | 21 | AAH81459  | Neisseria meningit  |
| 32 | 59.2  | 3.4  | 349980  | 21 | AAZ21609  | N. meningitidis B   |
| 33 | 59.2  | 3.4  | 1437668 | 21 | AAA81490  | Yeast AOD9604-asso  |
| 34 | 48    | 2.8  | 4590    | 22 | AAH24065  | Internal control B  |
| 35 | 43.2  | 2.5  | 14041   | 22 | AAH48024  | C. utilis crtB DNA  |
| 36 | 42.2  | 2.4  | 948     | 19 | AAV73180  | C. utilis crtB DNA  |
| 37 | 41.8  | 2.4  | 332     | 19 | AAV73190  | Sample Spurlina n   |
| 38 | 41.6  | 2.4  | 102     | 21 | AAZ59432  | DNA encoding lung   |
| 39 | 41.2  | 2.4  | 534     | 24 | ABK39272  | Signal transductio  |
| 40 | 41.2  | 2.4  | 11046   | 24 | ABK31537  | Human immune syste  |
| 41 | 40.8  | 2.4  | 6087    | 24 | ABL32418  | DNA encoding novel  |
| 42 | 40.6  | 2.3  | 330     | 23 | AA590678  | Chemically pretrea  |
| 43 | 40.4  | 2.3  | 7657    | 22 | AA545477  | Human immune syste  |
| 44 | 40.4  | 2.3  | 7657    | 24 | ABL34022  | Human immune syste  |
| 45 | 40.2  | 2.3  | 6078    | 24 | ABL33244  |                     |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AAI66366 |   |
| ID       | AAI66366 standard; cDNA; 1728 BP.   |
| XX       |   |
| AC       | AAI66366;   |
| XX       |   |
| DT       | 29-JAN-2002 (first entry)   |
| XX       |   |
| DE       | Nicotiana tabacum phytoene synthase coding sequence #1.                   |
| XX       |   |
| KW       | Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant; |
| KW       | plant growth regulator; herbicidal; tobacco; ss.                          |
| XX       |   |
| OS       | Nicotiana tabacum.  |
| XX       |   |
| FH       | Key   |
| FT       | CDS   |
| FT       | Location/Qualifiers   |
| FT       | 244..1566   |
| FT       | /*tag= a  |
| FT       | /product= "phytoene synthase"   |
| XX       |   |
| PN       | DE10022362-A1.  |
| XX       |   |
| PD       | 15-NOV-2001.  |
| XX       |   |
| PF       | 08-MAY-2000; 2000DE-1022362.  |
| XX       |   |
| PR       | 08-MAY-2000; 2000DE-1022362.  |
| XX       |   |
| PA       | (FARB ) BAYER AG.   |
| XX       |   |
| PI       | Busch M, Hain R;  |
| XX       |   |

DR WPI; 2002-027336/04.  
DR P-PSDB; AAM51841.

PT New nucleic acid encoding tobacco zeta-carotene desaturase, useful for  
PT screening compounds with herbicidal activity -

PS Claim 14; Page 12-17; 44pp; German.

The present invention provides the protein and coding sequences of phytoene synthases and zeta-carotene desaturase from *Nicotiana tabacum*. The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.

**SQ** Sequence 1728 BP; 513 A; 290 C; 433 G; 492 T; 0 other;

```
Query Match      100.0%; Score 1728; DB 24; Length 1728;
Best Local Similarity 100.0%; Fred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | AGAAACCCAGAAAGACACACAGGTTTTGCTTCTTGTTGATGAGTGCATTTGGCTCTGCTT  | 60  |
| DB | 1   | AGAAACCCAGAAAGACACACAGGTTTTGCTTCTTGTTGATGAGTGCATTTGGCTCTGCTT  | 60  |
| QY | 61  | GTGTAAAGCAAAGTCGGTTCACATTTCTATATCCGATTTTATAATCGTTGAAATTAGTG   | 120 |
| DB | 61  | GTGTAAAGCAAAGTCGGTTCACATTTCTATATCCGATTTTATAATCGTTGAAATTAGTG   | 120 |
| QY | 121 | GATAGACTCTAGTGGATATCTACAAGTATTGGTTTTTGTATATAATAGCTCAGGTTGAGA  | 180 |
| DB | 121 | GATAGACTCTAGTGGATATCTACAAGTATTGGTTTTTGTATATAATAGCTCAGGTTGAGA  | 180 |
| QY | 181 | AGGTAAACATAAAGGAAAGACAAAACCTTGGGAAATTGTTTAGACACACGAGGTTCTTCTT | 240 |
| DB | 181 | AGGTAAACATAAAGGAAAGACAAAACCTTGGGAAATTGTTTAGACACACGAGGTTCTTCTT | 240 |
| QY | 241 | TTCATGAGCATGCTGTTGCTTTGTTGTTGGGTTGTTTCTCCCACTTCCGAGGTCGCAAT   | 300 |
| DB | 241 | TTCATGAGCATGCTGTTGCTTTGTTGTTGGGTTGTTTCTCCCACTTCCGAGGTCGCAAT   | 300 |
| QY | 301 | GGGACAGGATTTGGATTTCAGTCCGAGAAAGGAAACCGCTCTTTGTATCATCCAGGTTTC  | 360 |
| DB | 301 | GGGACAGGATTTGGATTTCAGTCCGAGAAAGGAAACCGCTCTTTGTATCATCCAGGTTTC  | 360 |
| QY | 361 | CTAGCTCGAGATAGGAATTTGATGTGGATGGGAGATCAAGAAAGGTGGGAGACAAAGG    | 420 |
| DB | 361 | CTAGCTCGAGATAGGAATTTGATGTGGATGGGAGATCAAGAAAGGTGGGAGACAAAGG    | 420 |
| QY | 421 | TGGAAATTTTGGCTCTTTAAATGCTGATCCAAAGATATTCATGCTTGGTGGTGCATCAAGA | 480 |
| DB | 421 | TGGAAATTTTGGCTCTTTAAATGCTGATCCAAAGATATTCATGCTTGGTGGTGCATCAAGA | 480 |
| QY | 481 | GAAAGGGAAGACACTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCACGCTGGAGAAATG   | 540 |
| DB | 481 | GAAAGGGAAGACACTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCACGCTGGAGAAATG   | 540 |
| QY | 541 | ACTGTGTCATCAGAGAAAAAGGTGTATGATGTGGTATTAAGCAGGACGCTTTAGTGAAG   | 600 |
| DB | 541 | ACTGTGTCATCAGAGAAAAAGGTGTATGATGTGGTATTAAGCAGGACGCTTTAGTGAAG   | 600 |
| QY | 601 | AGGCAGCTGAGATCTACCGATGATTTAGAGTCAAGCCGAGATTTCTGTTCCAGGGAAT    | 660 |
| DB | 601 | AGGCAGCTGAGATCTACCGATGATTTAGAGTCAAGCCGAGATTTCTGTTCCAGGGAAT    | 660 |
| QY | 661 | TTGGGCTTGTGTAGTGAAGCATATGATCGTTGTGGGGAAGTATGTGCAGAGTATGCAAG   | 720 |
| DB | 661 | TTGGGCTTGTGTAGTGAAGCATATGATCGTTGTGGGGAAGTATGTGCAGAGTATGCAAG   | 720 |
| QY | 721 | ACATTTTACTTAGAACCAAGCTAATGACCCCAAGAGAGAAAGAGCTATCTGGGCAATA    | 780 |
| DB | 721 | ACATTTTACTTAGAACCAAGCTAATGACCCCAAGAGAGAAAGAGCTATCTGGGCAATA    | 780 |

XX Phytoene synthase coding sequence from N. tabacum.  
 DE  
 KW Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;  
 KW ultra violet absorber; food colour; ss.  
 XX  
 OS Nicotiana tabacum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 367..1599  
 FT /\*tag= a  
 XX  
 XX US5705624-A.  
 XX  
 PD 06-JAN-1998.  
 XX  
 XX 27-DEC-1995; 95US-0579667.  
 XX  
 XX 27-DEC-1995; 95US-0579667.  
 XX  
 PA (DELL/) DELLA-CIOPPA G R.  
 PA (FITZ/) FITZMAURICE W P.  
 PA (GRIL/) GRILL L K.  
 PA (HELL/) HELLMANN G M.  
 PA (KUNA/) KUMAGAI M H.  
 XX  
 PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;  
 PI Kumagai MH;  
 XX  
 XX WPI: 1998-086196/08.  
 DR P-PSDB; AAW41059.  
 XX  
 XX DNA encoding tobacco phytoene synthase polypeptides - useful for  
 PT producing recombinant polypeptides or transgenic plants  
 XX  
 XX Claim 1; Column 27-30; 25pp; English.  
 XX  
 CC This sequence encodes the phytoene synthetase from Nicotiana tabacum.  
 CC The phytoene synthetase coding sequence represents a cDNA of the  
 CC invention. The isolated nucleic acid molecules are used for producing  
 CC recombinant polypeptides or transgenic plants with enhanced ability to  
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber  
 CC and other carotenoids have been used as food colours, animal feeds and in  
 CC the pharmaceutical and cosmetics industries.  
 XX  
 XX Sequence 1826 BP; 589 A; 282 C; 433 G; 522 T; 0 other;  
 SQ

Query Match 50.2%; Score 868; DB 19; Length 1826;  
 Best Local Similarity 77.2%; Pred. No. 3.5e-237;  
 Matches 1187; Conservative 0; Mismatches 255; Indels 96; Gaps 7;

QY 109 TTGAATATTAGTGTAGTACTCTAGTGGATATCTACAGTATTGGTTTGTGTAATAATAG 168  
 DB 221 TAGACTCTAGTGGGATCTACTAGGAGTATTTTATTTTATTTTATTTTATTTTAAATAA 280  
 QY 169 GCTGAGGTGAGAGTAAACATAA-----GGAACACAAAAAATCTGGGAATGTGTTT 220  
 DB 281 GCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 340  
 QY 221 AGACACCCAGGTTCTCTTTTCATGAGCATCTGTGCTTTGTGTTGGTGTGTTCTC 280  
 DB 341 AGACACCCAGGTTTGTGTTCTC---AGAAATGCTGTTGCCCTGTGTTATGTTGTTTAC 397  
 QY 281 CCACCTCCGAGTCTCGAATGGGACAGAGGATCTTGATTCAGTCCGAGAGGAGGAGGAGG 340  
 DB 398 ---CTTGTGAGGTCTCAATGGGACAGGATCTTGATTCAGTAAAGGAGGAGGAGGAGGAGG 454  
 QY 341 TCTTTGTATCATCCAGGTTCTCTAGTCCGAGATAGGAATTTGATGGAATGGGAATCA 400  
 DB 455 TTTTGGACTCGTCGAGG-----CATAGGAATTTAGTGTGCAATGAGAGNAICA 502  
 QY 401 AGAAGGTGGGACAGAGGTTGGCTCTTTAATGCTGATCCAGATATTCAT 460  
 DB 502 TTTTGGACTCGTCGAGG-----CATAGGAATTTAGTGTGCAATGAGAGNAICA 502

DB 503 AAAGAGGTGTGAACAAAGGTGGAAATTTTGG----- 533  
 QY 461 GCTTGGGTGGATCAAGAACTGAAAAGGGAAGCACTTTCTCTACAGTCCAGTTTGGTGG 520  
 DB 534 -----TTCCTGACGCTCGCATGGTGG 556  
 QY 521 CTAGCCCAAGCTGGAGAAAT---GACTGTGTCTATCAGAGAAAGGTGTATGATGTGGTAT 577  
 DB 557 CTACACCAACGGGAGAAATGGCGACAATCACAATCAGACAGAAAGGTTTATGATGTGGTAT 616  
 QY 578 TAAAGCAGCGACGCTTTAGTGAAGAGGAGCTGAGATCTACCGATGATTTAGAGTGAAGC 637  
 DB 617 TGAACAAGCAGCTTTAGTGAAGAGGAGCTGAGATCTACTGATGATTTAGAGTGAAGC 676  
 QY 638 CGGATATTGTTGTTCCAGGGAATTTGGGCTGTTGAGTGAAGCATATGATCGTTTGGGG 697  
 DB 677 CGGATATCCCTCTCCCGGGAATTTGAGCTGTTAAGTGAAGCATATGATGATGTGATG 736  
 QY 698 AAGTATGTCAGAGTATGCAAGACATTTTACTTAGGACCAAGCTAATGACCCAGAGA 757  
 DB 737 AAGTATGTCAGAGTATGCAAGACATTTTACTTAGGAACTATGCTAATGACTCCAGAGA 796  
 QY 758 GAAGNAGAGCTATCTGGGCAATATATGCTGCTGAGGAGAACGGATGAGCTTGTGTATG 817  
 DB 797 GAAGAAGGCTATTGTTGGCAATATATGCTGCTGAGGAGAACAGATGAACTTGTGTATG 856  
 QY 818 GCCCTAATGCTATCCACATTAATCCGAACTTTAGTAGTGGGAGACAGGCTGGAAG 877  
 DB 857 GCCCAATGCTATCACAATATCTCCACAGCCTTAGATAGTGGGAGACGCTGGAAG 916  
 QY 878 ATATTTTCAGTGGCGGCAATTTGATATGCTTGTGCTGCTTTATCCGATCTGCTCCA 937  
 DB 917 ATGTTTTTCAGTGGCGGCAATTTGATATGCTGCTGCTTTGTCGATCTGTTTCCC 976  
 QY 938 GATTTCTCTGTTGATATTCAGCATTTCAGAGATATGATTGAAGAAATGCGTATGGACTTGT 997  
 DB 977 AGTTTCCAGTTGATATTCAGCCTTTCAGAGATATGATTGAAGAAATGCGTATGGACTTGA 1036  
 QY 998 GAAATTCAGATACAAAACTTTCGATGAGCTATATCTCTATTGTTTACTTGTGCTGGTA 1057  
 DB 1037 GAAATTCAGATACAAAACTTTCGATGAGCTATATCTCTATTGTTTACTTGTGCTGGTA 1096  
 QY 1058 CTGTAGGATTTGATGAGTGTCCAGATTATGGGTATGTCACCTGAATCAAGGCAACACAG 1117  
 DB 1097 CGTTTGGTGTGATGAGTGTCCAAATTTATGGGTATTGCACCTGATTCAAGGCAACACAG 1156  
 QY 1118 AGAGTGTATATAATGCTGCTTTGGCTTTAGGCTTGCATAATCAACTAACAATATACTCA 1177  
 DB 1157 AGAGTGTATATAATGCTGCTTTGGCTTTAGGATCGCAAAATCAACTAACAATATACTCA 1216  
 QY 1178 GAGATGTAGGAGAAAGATCCAGAGGAGGAGATATACCTTGCCTCAAGATGAATTAGCAC 1237  
 DB 1217 GAGATGTAGGAGAAAGATCCAGAGGAGGAGATGCTTACTTACCTCAAGATGAGTTAGCAC 1276  
 QY 1238 AGCAGGCTCTCCGACGAGACATATTTGCTGGAAGAGTGAATGAGTGGAGAACT 1297  
 DB 1277 AGCAGGCTCTCCGACATGACATTTTGTGCTGGAAGAGTGAATGAGTGGAGAACT 1336  
 QY 1298 TTATGAAGAAACAAATTCAGAGGCGGAGGAAATCTTTGATGAGTGAAGTGAAGGAGTGTCA 1357  
 DB 1337 TTATGAAGAAACAAATTCAGAGGCGGAGGAAATCTTTGATGAGTGAAGTGAAGGAGTGTCA 1396  
 QY 1358 CAGAACTGAGCTCTCTAGTATGCTGTGTTACAGGCTGCTGTTCTGATCGCAAGA 1417  
 DB 1397 CACAACTGAGCTCAGCTAGTATGCTGTATGCTGCTGTTGTTGTTGCTGCTGCTGCTG 1456  
 QY 1418 TATTGGACGAGATTGAAGCCACAGCTACAACTTCAAGAGGAGGCTTATGTTAGCA 1477  
 DB 1457 TACTCGACGAGATTGAGCCATGACTACAACTTCAAGAGGAGGCTTATGTTAGCA 1516  
 QY 1478 AGCCAAAGAGCTTCTACCTTGGCCCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1537  
 DB 1517 AACCAAGAGCTAATTTCTCTTACCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1576

QY 1538 GAAC-TCTCTCCACTAGCAAGACATGAATGAAGTAGTGTAGTCAATGAGTATATAC 1596  
 DB 1577 GAAC-TCTGTGACCTCTAGCTAGGCATAGACATCAGATTAATTAAGCAAGAAAGCA 1636  
 QY 1597 ACTAAGAAACTCAGGTACTTGTAAATGAGATATCTTT 1634  
 DB 1637 TATATTATTATTATATCTGTAAAGGAAAGAAATTT 1674

## RESULT 3

AAV03878  
 ID AAV03878 standard; cDNA; 1795 BP.

XX AC AAV03878;

XX DT 29-APR-1998 (first entry)

XX DE Phytoene synthase coding sequence from *N. benthamiana*.

XX KW Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;  
 ultra violet absorber; food colour; ss.

XX OS *Nicotiana benthamiana*.

XX FH Key Location/Qualifiers  
 FT CDS 361..1594  
 FT /\*tag- a

XX PN US5705624-A.

XX PD 06-JAN-1998.

XX PF 27-DEC-1995; 95US-0579667.

XX PR 27-DEC-1995; 95US-0579667.

XX PA (DELL/) DELLA-CIOPPA G R.

XX PA (FITZ/) FITZMAURICE W P.

XX PA (GRIL/) GRILL L K.

XX PA (HELL/) HELLMANN G M.

XX PA (KUNA/) KUMAGAI M H.

XX PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;  
 PI Kumagai MH;

XX DR WPI; 1998-086196/08.

XX DR P-PSDB; AAW41057.

XX PT DNA encoding tobacco phytoene synthase polypeptides - useful for  
 producing recombinant polypeptides or transgenic plants

XX PS Claim 1; Column 15-20; 25pp; English.

XX CC This sequence encodes the phytoene synthetase from *Nicotiana benthamiana*.  
 CC The phytoene synthetase coding sequence represents a cDNA of the  
 CC invention. The isolated nucleic acid molecules are used for producing  
 CC recombinant polypeptides or transgenic plants with enhanced ability to  
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber  
 CC and other carotenoids have been used as food colours, animal feeds and in  
 CC the pharmaceutical and cosmetics industries.

XX SQ Sequence 1795 BP; 577 A; 271 C; 434 G; 513 T; 0 other;

Query Match 49.7%; Score 858.6; DB 19; Length 1795;  
 Best Local Similarity 76.4%; Pred. No. 1.7e-234;  
 Matches 1230; Conservative 0; Mismatches 274; Indels 107; Gaps 10;

QY 141 TACAGTATTGTTTTTGTAAATAGCTGAGTGAGAGGTAACA-----TAAAG 193

DB 248 TAAATTTATTTATTTTATTAATTAAGGAGAGGAGGAGGAAACAACTGAAAG 307

QY 194 GAAACAAAAAATCTGGGAATTTTGTAGACCCAGCGAGTTCTTGTTCATGACATGT 253

DB 308 TAAGCAAAAAACCTTGGAAATTTTGTAGCAACCAAGGTTTTC--TTGCTCAGAAATGT 365  
 QY 254 CTGTTGCTTTGTTGTTGTTGTTTCTCCACTTCCGAGGTCTCGAATGGACAGGATTTG 313  
 DB 366 CTGTTGCCCTTGTATGGTTGTTTTCAC---CTTGTGAGGTCTCAAAATGGACAGGATTTCT 422  
 QY 314 TGGATTTCAGTCCGAGAAGAAACCGCTTTTGTATCATCCAGGTTCTAGTCCAGATA 373  
 DB 423 TGGATTCAATTCGGGAGGGAACCGGTTTGTATTTCTCGAGGT-----ATA 470  
 QY 374 GGAATTTGATGTGGAATGGGAATCAAGAAAGTGGGAGACAAAGGTGGAATTTTGGCT 433  
 DB 471 GAAATTTAGTGTCAATCAGAGGAACAAGAGAGTGGGAAACAAGGTGGAATTTTGG-- 528  
 QY 434 CTTTAAATGCTGATCCAAAGATATTTCATCTTGGGTGGATCAAGAACTGAAAAGGGAAGCA 493  
 DB 529 ----- 528  
 QY 494 CTTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCCCAGCTGGGCAAAAT---GACTGTGTCAT 550  
 DB 529 -----TTCTGTAGGTCTGCTATGTTGGCTACACCGCGGGGAGAAATGGCGAGATGACAT 584  
 QY 551 CAGAAAAAAGGTGTATGATGTGGTATTAAAGCAGGACAGCTTTAGTGAAGAGGCACTGA 610  
 DB 585 CAGAACAGATGGTTTATGATGTGGTTTAAACACAGCAGCTTTAGTGAAGAGGCACTGA 644  
 QY 611 GATCTACCGATGATTTAGAAAGTGAAGCCGGATATTGTTGTTCCAGGGAATTTGGGCTTGT 670  
 DB 645 GATCTACTGATGATTTAGAAAGTGAAGCCGGAGATCCCTCTCCAGCAAAATTTGAGCTTGT 704  
 QY 671 TGAGTGAAGCATATGATGCTGTGCGGAAGTATGTGAGAGTATGTCAGAGATGCAAGAGATTTTACT 730  
 DB 705 TGAGTGAAGCATATGATGAGTGTAGTGAAGTATGTCAGAGATGTCAGAGATTTTACT 764  
 QY 731 TAGGAACCAAGCTAATGACCCAGAGAGAAGAGAGCTATCTGGGCAATATATGTGTGT 790  
 DB 765 TAGGAACCATGCTAATGACTCCAGAGAGAAGAGGCTATTTGGGCAATATATGTATGT 824  
 QY 791 GCAGAGAACGGATGAGCTTGTGTATGGCCCTTAATGATCCACATACTCCGCAAGCTT 850  
 DB 825 GCAGAGAACAGATGAACCTTGTGTATGGCCCAATGATCCCATATTTACCCCAAGGCT 884  
 QY 851 TAGATAGTGGGAGACACCGCTGGAAGATATTTTCACTGGGCGGCCATTTGATATCTGTG 910  
 DB 885 TAGATAGTGGGAGACACCTGCTGGAAGATGTTTTCACTGGGCGGCCATTTGATATCTGTG 944  
 QY 911 ATGCTGCTTTATCCGATAGTCTCCAGATTTCTCTGTGATATTCAGCCATTCAGAGATA 970  
 DB 945 ATGCTGCTTTGTCGATAGTCTTCCAGTTTCCAGTTGATATTCAGCCATTCAGAGATA 1004  
 QY 971 TGATTGAAGGAATGCGTATGGACTTTGGAATCCAGATACAAACTTTTCATGAGCTAT 1030  
 DB 1005 TGATTGAAGGAATGCGTATGGACTTTGAGGAAGTCAAGATACAGAACTTTGATGAGCTAT 1064  
 QY 1031 ATCTCTATTGTACTATGTTGCTGTACTGTAGGATTTGATGAGTGTTCAGTTATGGGTA 1090  
 DB 1065 ACCTATATTGTTATACGTTGCTGTACGGTTGGGTGATGAGTGTTCGAATTTATGGGTA 1124  
 QY 1091 TTGCACCTGGAATCAAGGCAACAACAGAGAGTGTATATATCTGCTTTGGCTTTTAGGGC 1150  
 DB 1125 TTGCACCTGGAATCAAGGCAACAACAGAGATGTATATATGACGCTTTGGCTTTGGGTA 1184  
 QY 1151 TTGCAATCAACTAACCAATATCTACAGATGTAGGAGAAGATGCCAGAAGAGGAAG 1210  
 DB 1185 TAGCAATCAACTAACCAATATCTACAGATGTAGGAGAAGATGCCAGAAGAGGAAG 1244  
 QY 1211 TATACTTCCCTCAAGATGAATTTAGCACAGGCGAGGCTCTCCGACGAAGACATATTTGCTG 1270  
 DB 1245 TCTACTTACCTCAAGATGAATTTAGCACATGCAAGTCTCTCCGACGATGACATATTCGCTG 1304  
 QY 1271 GAAGAGTCACTGATTAAGTGGAGAACTTTTGAAGAAACAATTCAGAGGGGCGAGAAAT 1330



Db 1034 TTACCTCTATTGTTATTACGTTGCTGTACGGTTGGGTGATGAGTCTTCCAATTATGGG 1093  
 QY 1089 TATTGCACCTGAATCAAGGCAACACAGAGAGTATATAAGTCTGCTTTGGCTTTAGG 1148  
 Db 1094 TATTGCACCTGATTCAAGGCAACACAGAGAGCTATATAAGTCTGCTTTGGCTTTAGG 1153  
 QY 1149 GCTTGCAAACTCAACTAACCTATACCTACAGAGATGTAGGAGAGATCCAGAGAGGAAG 1208  
 Db 1154 AATGCGAATCACTAAGACATACCTACAGAGATGTAGGAGAGATCCAGAGAGGAAG 1213  
 QY 1209 AGTATACCTGCTCAAGATGAATTAGCAGGAGGCTCTCCGACGAAGACATATTGTC 1268  
 Db 1214 AGTCTACTTACCTCAAGATGAATTAGCAGGAGGCTCTCTCGACGATGACATATTGTC 1273  
 QY 1269 TGGAGAGTACTGATTAAGTGGAGGAACCTTATGAAGAAACAATTCAGAGGGGAGGAA 1328  
 Db 1274 TGSAAAGTACTGATTAAGTGGAGAGCTTTATGAAGAAACAATTCAGAGGGGCAAGAA 1333  
 QY 1329 ATTCTTTGATGAGTCAGAGAAAGGTGCACAGAACTGGACTCTGCTAGTAGTGGCCTGT 1388  
 Db 1334 GTTCTTGTGAGGACAGAGGAGGATACAACTAGCTACGCTACGAGATGGCCTGT 1393  
 QY 1389 GTTAACAGCCTGCTGTGTATCGCAAGATATTGGACGAGATTGAAGCCACGACTACAA 1448  
 Db 1394 ATGGGCATCTTTGCTGTGTACCGCCAAATACTGGACGAGATTGAAGCCATGACTACAA 1453  
 QY 1449 CAACCTCACAAGGAGGCTTATGTAGCAAGCCAAAGAGCTTCTACCTTGGCCATTGC 1508  
 Db 1454 CAACCTCACAAGGAGGCTTATGTAGCAAGCCAAAGAGCTTATTTCTTACCTATTGC 1513  
 QY 1509 TTATGCAAAATCTCTGTGCCCCCTAATAGAACT-TCCTCTCCACTAGCAAGACATGAA 1567  
 Db 1514 TTATGCAAAATCTCTGTGCCCCCTAAGAACTCTTGTACCTCTAGCTAAGGCATAGA 1573  
 QY 1568 TGAAGTAGTGTAGTCAATGATATTATACACTA----AAGAACTCAGGTACTTGTAAAT 1623  
 Db 1574 CATCAGATTTAAATTAAGCAAGAAAGCATATACCTGTTAAAGAAAGATTTCTTAAG 1633  
 QY 1624 GAGATATCTTT-----TGTAAATGTATCATCAAAAGTAGATTGT-AAATTCATA 1675  
 Db 1634 TAGATATTGTTGATGATGACCTTGTATATCATCAAAAGTAGGTAGTAAATCCATA 1693  
 QY 1676 TGACAATCTCTTG 1688  
 Db 1694 TAACAATCTCTAG 1706

## RESULT 5

AAV03881  
 ID AAV03881 standard; cDNA; 1814 BP.  
 XX  
 AC AAV03881;

XX  
 DT 29-APR-1998 (first entry)

XX  
 DE Phytoene synthase coding sequence from N. tabacum.

XX  
 KW Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;  
 KW ultra violet absorber; food colour; ss.

XX  
 OS Nicotiana tabacum.

XX  
 FH Key Location/Qualifiers  
 FT CDS 363..1595  
 FT /\*tag= a

XX  
 PN US5705624-A.

XX  
 PD 06-JAN-1998.

XX  
 PF 27-DEC-1995; 95US-0579667.

XX

PR 27-DEC-1995; 95US-0579667.  
 XX  
 PA (DELL/) DELLA-CIOPPA G R.  
 PA (FITZ/) FITZMAURICE W P.  
 PA (GRILL/) GRILL L K.  
 PA (HELL/) HELLMANN G M.  
 PA (KUMA/) KUMAGAI M H.  
 XX  
 PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;  
 PI Kumagai MH;  
 XX  
 WPI; 1998-086196/08.  
 DR P-PSDB; AAW41060.  
 XX  
 PT DNA encoding tobacco phytoene synthase polypeptides - useful for  
 PT producing recombinant polypeptides or transgenic plants  
 XX  
 PS Claim 1; Column 33-36; 25pp; English.  
 XX  
 CC This sequence encodes the phytoene synthetase from Nicotiana tabacum.  
 CC the phytoene synthetase coding sequence represents a cDNA of the  
 CC invention. The isolated nucleic acid molecules are used for producing to  
 CC recombinant polypeptides or transgenic plants with enhanced ability to  
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber  
 CC and other carotenoids have been used as food colours, animal feeds and in  
 CC the pharmaceutical and cosmetics industries.  
 XX  
 SQ Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;  
 Query Match 49.4%; Score 853.4; DB 19; Length 1814;  
 Best Local Similarity 76.5%; Pred. No. 5.2e-233;  
 Matches 1223; Conservative 0; Mismatches 266; Indels 110; Gaps 10;  
 QY 141 TACAAGTATTGGTTTTTGTATAAATAGCTGAGTGAGAGG-----TAACATAAAG 193  
 Db 250 TAAATTTATTAAATTTTATAAATTAAGCAGAGAGGAAGAAACAGAAACAGAAAG 309  
 QY 194 GAAGACAAAACCTGGGAATTTTAGACCACCGAGGTTTCTTGTTCATGAGCATGT 253  
 Db 310 TAAGACAAAACCTGGGAATTTTAGAAAACCAAGGTTTCTCTGTCTCAAA---ATGT 366  
 QY 254 CTGTTGCTTTGTTGGGTTGTTTCCACTCCGAGGCTCGAATGGGACAGGATTGT 313  
 Db 367 CTGTTGCTTTGTTGGGTTGTTTCCAC---CTTGTGAAGTCTCAATGGGACAGGATTCT 423  
 QY 314 TGGATTCACTCCGAGAGAAACCGCTTCTTTGATCATCCAGGTTCTAGCTCGAGATA 373  
 Db 424 TGGATTCACTCCGAGAGAAACCGGTTTGTGATTCGTCGAGG-----CATA 471  
 QY 374 GGAATTTGATGTGGAATGGGAGAAATCAAGAAGGTGGGAGACAAAGTGGAAATTTGGCT 433  
 Db 472 GGAATTTGATGTGGAATGGGAGAAATCAAGAAGGTGGGAGAGGTTGGAATTTTGG-- 529  
 QY 434 CTTTAATTTGCTGATCCCAAGATATTTCATCTTGGGTGGATCAAGAACTCAAAAGGGAAGCA 493  
 Db 530 ----- 529  
 QY 494 CTTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCAGCTGGAGAAAT---GACTGTGTCTAT 550  
 Db 530 ----TTCGTGAAGTCTGCTATGTTGGCTACACCGCGGGAGAAATGCGGACGATGACAT 585  
 QY 551 CAGAGAAAAGGTGTATGATGTGTTATTAAGCAGGAGGCTTTAGTGAAGAGGCGAGCTGA 610  
 Db 586 CAGAACAGATGGTTTATGATGTGTTTATAAACAGCAGCTTTAGTGAAGAGGCGAGTTGA 645  
 QY 611 GATCTACCGATGATTTAGAAGTGAAGCGGATATTGTTTCCAGGGGAATTTGGCCTGT 670  
 Db 646 GATCTGCTGATGATTTAGAAGTGAAGCGGAGATCCCTCTCCCGGGGAATTTGACCTGT 705  
 QY 671 TGAGTGAAGCATATGATCGTTTGTGGCGAAGTATGTGCAAGATATGCAAAAGACATTTTACT 730  
 Db 706 TGAGTGAAGCATATGATAGGTGTAGTGAGGTATGTGCAAGATATGCAAAAGACATTTTACT 765

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OY 731 TAGGAACCAAGCTAATGACCCAGAGAGAGAGAGAGAGAGCTATCTGGCAATATATATGTGGT 790
DB 766 TAGGAACCAAGCTAATGACCTACGAGAGAGAGAGAGAGAGCTATCTGGCAATATATATGTGGT 825
OY 791 CGAGAGAACGATGAGCTTCTGATGCCCTAATGATCCACATACCTCCGCAAGCTT 850
DB 826 CGAGAGAACGATGAGCTTCTGATGCCCTAATGATCCACATACCTCCGCAAGCTT 885
OY 851 TAGATAGTGGGAGACGAGCTGGAAGATATTTTCAGTGGGCGGCATTTTCATATGCTTG 910
DB 886 TAGATAGTGGGAGACGAGCTGGAAGATATTTTCAGTGGGCGGCATTTTCATATGCTTG 945
OY 911 ATGTGCTTTATCCGATATCTCTCCAGATTTCTGTTGATPATTACGCCATTCAGAGATA 970
DB 946 ATGTGCTTTATCCGATATCTCTCCAGATTTCTGTTGATPATTACGCCATTCAGAGATA 1005
OY 971 TGATTGAAGGAATCGGTATGACCTTGTGGAAATCCAGATACAAAACITTCATGAGCTAT 1030
DB 1006 TGATTGAAGGAATCGGTATGACCTTGTGGAAATCCAGATACAAAACITTCATGAGCTAT 1065
OY 1031 ATCTCTATTGTTACTATCTGCTGCTAGTGTAGGATTTGATGAGTGTTCACGTTATGGTA 1090
DB 1066 ACCCTATTGTTACTATCTGCTGCTAGTGTAGGATTTGATGAGTGTTCACGTTATGGTA 1125
OY 1091 TTGCACCTGATCAAGGCAACACAGAGAGTGTATATTAATGCTTTGCTTTAGGGC 1150
DB 1126 TTGCACCTGATCAAGGCAACACAGAGAGCGTATATTAATGCTTTGCTTTAGGAA 1185
OY 1151 TTGCAATCAACTACCACTATCTACAGATGTAGGAGAGATGCCAGAGAGAGAG 1210
DB 1186 TCGCAATCAACTACCACTATCTACAGATGTAGGAGAGATGCCAGAGAGAGAG 1245
OY 1211 TATACCTGCCCAAGATGATGATGACAGAGCGGCTCTCCGAGCAACATATTTGCTG 1270
DB 1246 TCTACTACCTCAAGATGATGATGACAGAGCGGCTCTCTCGAGTACATATTTGCTG 1305
OY 1271 GAAGAGTACATGATAGTGGAGAGACTTTATGAGAAACAAATTCAGAGGGCGAGGAAT 1330
DB 1306 GAAAGTACATGATAGTGGAGAGACTTTATGAGAAACAAATTCAGAGGGCGAGGAAT 1365
OY 1331 TCTTTGATGAGTACAGAGAAAGGTGTCAGAGAGTGGACTCTGCTAGTAGAGTGGCTGCT 1390
DB 1366 TCTTCGATGAGGAGAGAGAGAGGATGATACAACTGAGTACAGTACAGATGGCTGAT 1425
OY 1391 TAACAGCGCTGCTGTTGATCCAGATATTTGGAGAGATTTGAGCCCAACGACTACACA 1450
DB 1426 GGGCATCTTTGCTGTTGATCCGCAATTAATCTGGAGAGATTTGAGCCCAATGACTACACA 1485
OY 1451 ACTTCAGAGAGGCGCTTATGTTAGCAAGCAAGAGAGCTTCTACCTTGGCCATTTGCTT 1510
DB 1486 ACTTCAGAGAGAGGCTTATGTTAGCAAGCAAGAGAGCTTATTTCTTACCTATTGCTT 1545
OY 1511 ATGCAAAATCTCTGTCGCCCTTAATCAACT-TCCTCTCCACTAGCAAGAGACATGATG 1569
DB 1546 ATGCAAAATCTCTGTCGCCCTTAATCAAGAGAGCTTGTCACTCTAGCTAGGCTAGACA 1605
OY 1570 AAGTAGTTGAGTCAATG-----AGTATTATACACTAAAGAACTCAGGTACTTGTAAA 1622
DB 1606 TCAGATTTAAATTAAGCAAGAAACCATATATTACTATTAAAGAAAGATTTCTAAA 1665
OY 1623 TGAGATATCTTT-----TGCTAAATGTATCATCAAAAGAGTAGATGTT-AAATCAAT 1674
DB 1666 GTAGATATTTGTTGATGATGCGCACTGTATATCATCAAAAGTAGTAGTAAATCCAAAT 1725
OY 1675 ATGCAAACTCTGTTAGTAATATTTTCCACACTATC 1713
DB 1726 ATAACAATCTCTAGTAGTGTGATGTTCAATCTTTAAGC 1764
```

RESULT 6

AAQ99323

ID AAQ99323 standard; cDNA; 1591 BP.

XX

AAQ99323;

13-APR-1996 (first entry)

Melon phytoene-synthase gene.

melon; phytoene-synthase; ripening; cDNA library; fruit; MEL5;  
tomato; TOM5; probe; hybridisation; polymerase chain reaction; PCR;  
antisense; transgenic plant; crop improvement; carotenoid; vector;  
ss.

Cucumis melo.

WO9602650-A2.

01-FEB-1996.

06-JUL-1995; 95WO-GB01603.

22-SEP-1994; 94GB-0019081.

18-JUL-1994; 94GB-0014505.

(ZENE) ZENECA LTD.

Grierson D, John I, Karvouni Z, Taylor J, Turner A;

Watson C;

WPI; 1996-105912/11.

New isolated DNA encoding melon phytoene synthase - used to  
transform plants to modify carotenoid content and related  
characteristics in plant parts, partic. fruit

Claim 2; Page 15-16; 22pp; English.

The sequence encodes melon phytoene-synthase (MEL5 gene), and is  
almost full-length. The sequence has been isolated as a cDNA clone  
from a ripening-related cDNA library derived from climacteric melon  
fruit, using the tomato phytoene-synthase cDNA (TOM5) as a  
heterologous probe. The MEL5 gene 5'-end has also been isolated by  
polymerase chain reaction and sequenced. The DNA may be used in  
sense or antisense constructs to modify gene expression in plants.  
The carotenoid content and related characteristics of plant parts  
(particularly fruit) may be modified in this way.

Sequence 1591 BP; 507 A; 237 C; 395 G; 452 T; 0 other;

Query Match 49.1%; Score 847.6; DB 17; Length 1591;

Best Local Similarity 77.6%; Pred. No. 2.2e-231;

Matches 1136; Conservative 0; Mismatches 249; Indels 79; Gaps 6;

OY 101 TATATCTCTGAAATTTAGTGGATAGACTCTAGTGGATATCTAC---AAGTATTGGTGT 157

DB 116 TAAATTTGTTGAGAGTGGAAATATCTCTAGTGGAAATCTACTAGGATTAATTTATTT 175

OY 158 TGATAAATAGCTCAGGTGAGAAGTAACTAAAGAAAGACAAAACCTTGGGAATGT 217

DB 176 CTATAAATAGTAAAGTTTGAAGGTGACA-AAAAGAAAGACAAAATCTTGAATGT 234

OY 218 TTTAGACACCGAGGTTTCTTTTCATGAGCATGCTCTGTTGTTGTTGGTGTGTTT 277

DB 235 TTTAGACAACCAAGGT---TTTCTTGTCTCAGAATGCTCTGCTTGTATGGTGTGTTT 291

OY 278 CTCCCACTCCGAGGCTCGAATGGACAGAGATTTGATTCAGTCCGAGAGGAAC 337

DB 292 CTC---CTGTGACGCTCAAAATGGACAAGTTTTCATGGAATCAGTCCGAGGGAAC 348

OY 338 GCGTCTTTGATCATCCAGGTTCTTAGCTCGAGATAGGAATTTGATGTGGAATGGAGAA 397

DB 349 GTTTTTTGTATCATCGAGG-----CATAGGAATTTGTTGTTCAATGAGAGAA 396

OY 398 TCAAGAAAGGTGGGAGACAAGGTGGAATTTTGGCTCTTTAATTTGCTGATCCAGATATT 457

Db 397 TCAATAGAGT----- 407  
Qy 458 CATGCTGGTGGATCAAGAACTGAAAGGGAAGCACTTTCTGTACAGTCCAGTTGG 517  
Db 408 -----GGTGAAGCAAACTAATAATGACGGAATTTCTGTACGGTCTGCTATTT 459  
Qy 518 TGSCTAGCCAGCTGGAGAAATGACTGTGTCATCAGAGAAAAGGTGTATGATGTGAT 577  
Db 460 TGGTACTCCATCTGGAGAACGGAGATGACATCGGAACAGATGGTCTATGATGTGTT 519  
Qy 578 TAAAGCAGCAGCTTTAGTGAAGAGGAGCTGAGATCTACCGATGATTTAGAACTGAAGC 637  
Db 520 TGAGCAGCAGCTTGGTGAGAGGCACTGAGATCTACCAATGAGTTAGAGTGAAGC 579  
Qy 638 CGGATATTTGTTCCAGGGAATTTGGGCTTTGTTGAGTGAAGCATATGATCGTTGGCG 697  
Db 580 CGGATATACCTATTCCGGGGAATTTGGCTTGTGAGTGAAGCATATGATAGTGTGGTG 639  
Qy 698 AAGTATGTCAGACTATGCAAGACATTTACTTTAGGACCACTAATGACCCAGAGA 757  
Db 640 AAGTATGTCAGATATGCAAGACGTTTAACTTTAGGAACTATCTAATGACTCCGAGA 699  
Qy 758 GAAGAAGAGCTATCTGGCCATATATGTGTGTCAGAGAACGATGAGCTTTGTATG 817  
Db 700 GAAGAGGCTATCTGGCCATATATGTGTGTCAGAGAACGATGAGCTTTGTATG 759  
Qy 818 GCCATATGCAATCCAGCACTCCGCAAGCTTTAGATGGTGGAGACCAAGGCTGGAAG 877  
Db 760 GCCCAAGCGCATATATATCCCGGAGCTTTAGATAGTGGGAAATAGGCTAGAAG 819  
Qy 878 ATATTTTCAGTGGCGGCACTTTGATATGCTGATGCTGTTTATCGATCTCTCCA 937  
Db 820 ATGTTTCAATGGCGGCACTTTGACATGCTGATGCTGTTTCTCCGATACAGTTCTA 879  
Qy 938 GATTTCCTGTTGATATTCAGCACTTCAGAGATATGATTTGAAGGAATCGTATGACTGT 997  
Db 880 ACTTTCAGTTGATATTCAGCCATTCAGAGATATGATTTGAAGGAATCGTATGACTGA 939  
Qy 998 GGAATCCAGATACAAACTTTTCGATGAGCTATATCTCTATTTGTTACTATGTTCTGGTA 1057  
Db 940 GAAATCCAGATACAAAACTTCGACGAATATACCTTTATTTGTTATTTATGTTCTGGTA 999  
Qy 1058 CTGTAGGATTCATGAGTGTTCACCTATGTTGATGTCACCTGATCAAGCAACACAG 1117  
Db 1000 CGTGTGGTGTGAGTGTTCCTAATATGTTGATGTCGCTGATCAAGCAACACAG 1059  
Qy 1118 AGAGTGTATATATGCTGCTTTGGCTTTAGGCTTTGCAAAATCAACTAACCAATATCTCA 1177  
Db 1060 AGAGCTATATATGCTGCTTTGGCTCTGGGATCGCAATCAATTAACATACTCA 1119  
Qy 1178 GAGATGTAGGAGAGATGCGAGAGAGAGATATCTTCCCTCAAGATGAATAGCAC 1237  
Db 1120 GAGATGTGGAGAGATGCGAGAGAGAGATCTTCTTCCCTCAAGATGAATAGCAC 1179  
Qy 1238 AGCAGGCTCTCCGACAGACATATTTGCTGGAAGATGACATGAAGTGGAGGACT 1297  
Db 1180 AGCAGGCTCTATCGATGAAGATATTTGCTGGAAGGATGACCTAATATGAGATCT 1239  
Qy 1298 TTATGAAGAAACAAATTCAGAGCGGAGGAATTTCTTTGATGATCAGAGAAAGGTGCA 1357  
Db 1240 TTATGAAGAAACAAATACATAGGCAAGAAAGTTCTTTGATGAGCAGAGAAAGCGTGA 1299  
Qy 1358 CAGAACTGGATCTGCTAGTAGATGCGCTGTGTTAAAGCGCTGCTGTTGATCGCAAGA 1417  
Db 1300 CAGAACTGGATCTGCTAGTAGATGCGCTGTGTTAAAGCGCTGCTGTTGATCGCAAGA 1359  
Qy 1418 TATTGGAGGATGTGAAGCCAACTACACAACTTCACAGAGGAGGCTTATGTAGCA 1477  
Db 1360 TACTAGATGAGTGAAGCCAACTGACTACAACTTCACAAAGAGGATATGTAGCA 1419  
Qy 1478 AGCCAAAGAGCTTCTCACCTTGGCCATTTGCTTATGAAATCTCTGTGCCCCCTAATA 1537  
Db 1420 AATCAAGAGATGTGATGCAATTAATGATGCAATGCAAAATCTCTGTGCTCTCTACAA 1479

Qy 1538 GAACTTCTCTCCACTAGCAAGA 1561  
Db 1480 AACTGCTCTCTCTCAAGATAAA 1503

RESULT 7  
AAQ12495  
ID AAQ12495 standard; cDNA; 1646 BP.  
XX AAQ12495;  
XX AC AAQ12495;  
XX 18-SEP-1991 (first entry)  
XX Tomato fruit ripening related gene pTOM5.  
XX ripening; lycopen; transgenic tomato; ss.  
XX Lycopersicon esculentum var. Allisa Craig.  
XX Key Location/Qualifiers  
FT CDS 201..1436  
FT /\*tag= a.  
XX W09109128-A.  
XX 27-JUN-1991.  
XX 10-DEC-1990; 90WO-GB01924.  
XX 13-DEC-1989; 89GB-0028179.  
XX (ICIL ) IMPERIAL CHEM INDS. PLC.  
XX Bird CR, Grierson D, Schuch W;  
XX WPI; 1991-208154/28.

DNA construct to modify synthesis of plant carotenoid(s) -  
comprises sequence homologous to gene of clone pTOM5 preceded by  
plant promoter

Disclosure; Fig 1; 35pp; English.

Clone pTOM5 was derived from a cDNA library isolated from ripe  
tomato RNA (Slater et al., Plant Molecular Biology 5, 137-147,  
1985). The protein it encodes is estimated to have mol. wt. ca.  
48kD. pTOM5 is expressed in ripening fruit. Strongest expression is  
at the full orange stage of ripening; no expression is detected in  
green fruit. See also AAQ12494.

XX Sequence 1646 BP; 529 A; 249 C; 387 G; 481 T; 0 other;

Query Match 48.68; Score 840.4; DB 12; Length 1646;  
Best Local Similarity 74.38; Pred. No. 2.5e-229;  
Matches 1221; Conservative 0; Mismatches 331; Indels 92; Gaps 9;

Qy 101 TATATCCTGTAATTTAGTGGATAGACTCTAGTGGATATCTAC---AAGTATTGCTTTT 157  
Db 53 TAATTTGTTGAGAGTGAATATTTCTAGTGGATCTACTAGGAGTATTTATTTT 112  
Qy 158 TGATAAATAGGCTGAGGTGAGAGGTAAACATAAGAGAAACAAAACTTGGGAATTGT 217  
Db 113 CTATAAACTAGTAAAGTTTGAAGGTGACA-AAAAGAAAGACAAAAATCTTGAATTGT 171  
Qy 218 TTTAGACCCAGCGGTTTCTTGTTCATGACATGCTCTGTTGCTTGTGTGGGTTGTT 277  
Db 172 TTTAGAACCAACAGGT---TTTCTTGTCTCAGATGCTCTGTTGCTTGTATGGGTTGTT 228  
Qy 278 CTCACCCTTCGAGGCTCTCGAATGGACAGGATTTCTGATTCAGTCCGAGAGCAACC 337  
Db 229 CTC---CTTGTGACGCTCTCAATGGACAAAGTTTTCATGGAATCAGTCCGGAGGAAACC 285



This sequence encodes the phytoene synthetase from *Nicotiana benthamiana*. The phytoene synthetase coding sequence represents a cDNA of the invention. The isolated nucleic acid molecules are used for producing recombinant polypeptides or transgenic plants with enhanced ability to synthesise carotenoids. Phytoene has been used as a ultra violet absorber

CC and other carotenoids have been used as food colours, animal feeds and in  
CC the pharmaceutical and cosmetics industries.

Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other;  
XX  
SQ

|                            |       |                     |            |              |
|----------------------------|-------|---------------------|------------|--------------|
| Query Match                | 46.9% | Score 811.2;        | DB 19;     | Length 1316; |
| Best Local Similarity      | 80.2% | Pred. No. 4.9e-221; |            |              |
| Matches 1039; Conservative | 0;    | Mismatches 173;     | Indels 84; | Gaps 4;      |

|    |     |  |     |
|----|-----|--|-----|
| Qy | 250 | ATGCTCTGTTGCTTTGTTGTTGGGTTGTTTCCTCCACATTCGAGTCTCGAATGGGACAGGA  | 309 |
| Db | 1   | ATGCTCTGCTTTGTTTATGGGTTGTTTTCAC---CTTGTGAGGTTCTCAAAATGGGACAGGA | 57  |
| Qy | 310 | TTGTTGGATTTCAGTCCGAGAGGAAACCGCGTCTTTGTATCATCCAGGTTCTTAGTCTGA   | 369 |
| Db | 58  | TTCTTGGATTCAATCCGGGAGGAAACCGGGTTTGTATTGGTCTGAGG-----           | 105 |
| Qy | 370 | GATAGGAATTTGATGTGGAAATGGGAGAATCAAGAAAGGTGGGAGACAAAGGTGGAATTTT  | 429 |
| Db | 106 | CATAGGAATTTAGTGTGCAATGAGAGAAACAAGAGAGAGGTGTGTGGAACAATGCGAATTTT | 165 |
| Qy | 430 | GGCTCTTAATTGCTGATCCAGATATTATGCTTGGTGGATCAAGAAGTGAAGAAAGGA      | 489 |
| Db | 166 | GGTCTCTGTA-----  | 175 |

Qy 490 AGCATTCTCTGACAGTCCAGTTGGTGGTAGCCAGCTGGAGAAAT--GACTGTG 546  
Db 176 -----AGCTGCTATGGTGGCTACCGCGGGGAGAGAAATGGCGACGATG 219

QY 547 TCATCAGAGAAAAAGGTGTATGATGTGGTATTAAAGCAGGCAGCTTTAGTGAAGAGGCAG 606

Db 220 ACATCAGAACAGATGGTTTATGATGTGGTATTGAACAAACAGCTTTAGTGAAGAGGCAG 279

|                      |  |     |
|----------------------|--|-----|
| <b>Qy</b>            | 607 CTGAGATCTACCGATGATTAGAGTGAAGCCGGATATTGTTCACGGGAATTGGGC         | 666 |
|                      |  |     |
| <b>D<sub>b</sub></b> | 280 TTGAGATCTACTGTGATGATTAGAACTGAAGCCGGCAGATCCCCTCCCGGGCAATTTTCAGC | 329 |

|    |     |  |     |
|----|-----|--|-----|
|    | 667 | TGTTTGAAGCATATGTCTCGTTGGCAAGTAGTGTCAGAAGTATGCAAAGACATT | 726 |
| QY |     |  |     |
|    | 340 | TTGTTGACTGAGCAGCATATGATAGGTTAGCCAGGTAATCTGCCAAGCACATTT | 398 |
| Dd |     |  |     |

[illegible]

Qy 787 TGGTGCAGGAGAACGGATGAGCTTGTGATGGCCCTAATGCATCCACATACTCCGCA 846

QY 847 GCATTAGATAGTGGGAGACCAAGGCTGGAAGATATTTTCAGTGGGGGCCATTTCATATG 906

QY 907 CTTGATGCTGCTTTATCCGATACTGTCTCCAGATTTCTCTGTTGATATTACAGCCATTGAGA 966

967 GATATGATTGAAGGAATGGGTATGGACTTGTGGAAATCCAGATACAAAACCTTTTCGATGAG 102

DD 040 GATATGATCGAAGGAATGGTATGGACTTGGAGGAGTGGAGATACAGAACTTTGATGAG 699  
 QY 1027 CTATATCTTATTCTTACTATGTTGCTGGTACTGTAGGATTGATGAGTCTTCCAGTTATG 108

DB 700 CATAACCTATATCTTATTACGTTGGTGGTACAGTTGGGTTGATGAGTGTTCCCAATTATG 759

QY 1087 GGTATTGCACCTGTAATCAAGGCCAACACAGAGAGTGATATATAATGCTGCTTTGGCTTTA 114

Db 760 GGCATCGCACCCTGATCAAGGCAACACAGAGTCTATATATGACGCTTTGGCTTTG 819

Qy 1147 GGGCTTGCAAAATCAACTAACCAATATACTCAGAGATCTAGGAGAAGATGCCAGAAAGGA 120

Db 820 GGTATCGGGAATCAACTAACCACATTCTCAGAGATCTCGGAGAAGATGCCAGAGAGGA 879

|    |      |           |                       |                           |                            |      |
|----|------|-----------|-----------------------|---------------------------|----------------------------|------|
| Qy | 1207 | AGAGTATAC | TGGCTCAAGATGAAT       | TAGCACAGG                 | CAGGGCTCTCCGACGAAGACATATTT | 1266 |
|    |      |           |                       |                           |                            |      |
| Db | 880  | AGAGTCTAC | TTACCTCAAGATGAAT      | TAGCACAGG                 | CAGGCTCTCCGACGATGACATATTT  | 939  |
|    |      |           |                       |                           |                            |      |
| Qy | 1267 | GCTGGAAAG | TGACTGATTAAGTGGG      | AAGACTTTATGAGAAACAAT      | TCAGAGGGCGAGG              | 1326 |
|    |      |           |                       |                           |                            |      |
| Db | 940  | ACTGGAAAG | TGACTGATTAATGGG       | AAGACTTTATGAGAAAGCAAT     | TCAGAGGGCAAGA              | 999  |
|    |      |           |                       |                           |                            |      |
| Qy | 1327 | AAATCTCTT | GATCAGTCAGNAAGG       | TGCACAGAACTGG             | ACTCTGCTAGTAGATGGCCT       | 1386 |
|    |      |           |                       |                           |                            |      |
| Db | 1000 | AAGTCTTCA | ATGAGGCAGGAGGAG       | TTACACAACTGAGCT           | AGCTAGTCAGCAGATGGCCT       | 1059 |
|    |      |           |                       |                           |                            |      |
| Qy | 1387 | GTGTTAAAC | AGCGCTGCTGTTGTATCC    | AAAGATATGGACGAGATTGAAGC   | CAACGACTAC                 | 1446 |
|    |      |           |                       |                           |                            |      |
| Db | 1060 | GTATGGCAT | CTTTGCTTTGTACCGC      | CAATACTCTGCAGGAGATCGAAGCC | AACTGACTTAC                | 1119 |
|    |      |           |                       |                           |                            |      |
| Qy | 1447 | AACAAC    | TTACAAGGAGGCTTATGTTAG | CAGCCAAAGAGCTTCTCACCT     | TGCCCCATT                  | 1506 |
|    |      |           |                       |                           |                            |      |
| Db | 1120 | AACAAC    | TTACAAGAGAGCTTATGTG   | AGCAAAATCAAAGAGCTAAT      | TTCTCTACCTATT              | 1179 |
|    |      |           |                       |                           |                            |      |
| Qy | 1507 | GCTTATGCA | AAATCTCTTGTGCCCC      | CTAATAGA                  | ACT                        | 1542 |
|    |      |           |                       |                           |                            |      |
| Db | 1180 | GCTTATGCA | AAATCTCTTGTGCCCC      | CTAAGA                    | ACT                        | 1215 |
|    |      |           |                       |                           |                            |      |

RESULT 9  
AAZ99482

AAZ99482  
ID AAZ99482 standard; CDNA; 1239 BP.

AA  
AC AAZ99482:

XX 03-TU-30

XX

XX  
---  
exam, emphasizing a proficiency of numerical proficiency

KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;  
Gibberellic acid; copalyl diprenosylate synthase; 3beta-hydroxylase;  
KW seed germination; seedling growth; gibberellin biosynthetic pathway;  
KW transgenic plant; hypocotyl; epicotyl; ss.

YY Lycopersicon esculentum.

| XX | FH | Key | Location/Qualifiers |
|----|----|-----|---------------------|
|    |    |     |                     |

1.1239  
/44300 =

```

ET      /product= "phytoene synthase"

```

```
FT
    /transl_except= (pos: 1057..:1059, aa: Arg)
    /transl_except= (pos: 1057..:1059, aa: Arg)
```

AA  
PN  
WO200009722-A2XX  
PD  
24-FEB-2000

XX

XX  
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PK 10-AUG-1998; 9805-0096111  
PR 07-JUN-1999; 9905-0137977

XXXXX  
DPA  
(MONC  
' MONC  
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PI Pillar KJ, Rao S, Ream JE;

XX  
DR  
WPT: 2000-224351/19

DR P-PSDB; AAY84101.

PT Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone .

PS Claim 45; Page 254-255; 267pp; English.

CC The present sequence encodes a phytoene synthase polypeptide, which



CC The present sequence encodes phytoene synthase 4. It was isolated from  
CC a cDNA library prepared from mRNA extracted from the petals of *Gentiana*  
CC *lutea*. The nucleic acid sequence was amplified from the library using  
CC PCR primers AAV16952-53. The phytoene synthase gene is useful for  
CC breeding plants with variable flower colours.

Sequence 2868 BP; 887 A; 499 C; 648 G; 833 T; 1 other;

Query Match 40.1%; Score 692.4; DB 19; Length 2858;  
Best Local Similarity 73.6%; Pred. No. 6e-187;  
Matches 949; Conservative 0; Mismatches 311; Indels 30; Gaps 4;

|    |      |  |      |
|----|------|--|------|
| QY | 240  | TTTCATGACGATGTCGTGTTGGCTTTCTGTGGGGTGTGTTCTCCCACTTCCCGAGGTCCTCGAA | 299  |
| DB | 390  | TTCTGTATACATGTCTATATTGTGACGCTATGGGTGTTTTCGCGCGAGTCTCTGAAGTTTGTAG | 449  |
| QY | 300  | TGGGACAGGATTGTTGGATTTCAGTCCGAGAGGAAACCGCTCTTTGTATCATCCAGGTT      | 359  |
| DB | 450  | TGSCAATGTTTCTTGGGACCAATTCGAGAAAGTTACCAATTTTCG-----               | 495  |
| QY | 360  | CCTAGCTCGAGATAGGAATTTTGATGTGGAATGGGAGAAATCAAGAAAGGTGGGACACAAG    | 419  |
| DB | 496  | -----GATAAAAGTTTAATCTACAAATGGAAGAGCTTTAAGAAAGTAGACACCAAG         | 545  |
| QY | 420  | GTGGAAATTTTGGCTCTTAATTCGTGATCCCAAGATATTTCATGCTTGGGTGGGATCAAGAAC  | 479  |
| DB | 546  | GGCTAGATCACGTTATGGGGTTTGGAGATTGAGTTTCATTTTTCGTTAGAGAGATCTGGATT   | 605  |
| QY | 480  | TGAAA---AGGGAAGCAGCTTCTCTGTACAGTCCAGTTTGTGCTAGCCAGCTGCAGAGA      | 536  |
| DB | 606  | AGAGACCCCGGAGAGNAGTTATCGGTATCTCCNAGTATTATAGCTACCCCGGACGAGAGA     | 665  |
| QY | 537  | AATGACTGTGTCATCAGAGAAAAAGGTGTATGATGTGTTATTAAGCAGGACGAGCTTTAGT    | 596  |
| DB | 666  | AATGACGATGACATCAGAGCAAAAGGTTTATGATGTCGTTTAAAGCAAGCAGCTTTGAT      | 725  |
| QY | 597  | GAAGGGCAGCTGAGATCTACCGATGANTTTAGAAGTGAAGCCGGATATTGTTGTTCCAGG     | 656  |
| DB | 726  | TAATGACAGTTTGAGGCTTAGAGAAATTTGGAGGTGAACCGGACATATTATTTGCCAGG      | 785  |
| QY | 657  | GAATTTGGGCTGTTGAGTGAAGCATATGATCGTTGTGCGGAAGTATGTGCAGAGTAGTC      | 716  |
| DB | 786  | AAACGGACGCTGTGGAATGAAGCTTTATGTCGGTGCAGAAAGTATGTGCTGAATATGC       | 845  |
| QY | 717  | AAAGACATTTTACTTAGGAACCAAGCTAATGACCCAGGAGAGAAGAGAGCTATCTGGGC      | 776  |
| DB | 846  | CAAGTCATTCTACTGGGGAACCAAGCTCATGACACCGGAGAGGCGTTTAGCTATCTGGC      | 905  |
| QY | 777  | AATATATGTGTGTCGAGGAGAACCGATGAGCTTGTGATGGCCCTAATGCAATCCACAT       | 836  |
| DB | 906  | GATATATGATGTGTAGAGAGACAGATGAGCTTGTGATGGGCTACACGGCTCACACAT        | 965  |
| QY | 837  | AACCTCCGAAGCTTTAGATAGTGGAGACACAGGCTGGAAGATATTTTCAGTGGGCGGC       | 896  |
| DB | 966  | AAATCCAAACCGGTTAGATAGTGGGAAGCAAGATTAGAAGATGTTTCAAAGGGCAACC       | 1025 |
| QY | 897  | ATTGATATGCTTGATGCTGCTTTATCCGATACTGCTCCAGATTTCCTGTGTATATCA        | 956  |
| DB | 1026 | TTTTGATATGCTTGATGCTGCTTTATCTGATACCAATTACCAAGTATCCTGTGGACATCCA    | 1085 |
| QY | 957  | GCCATTCAGAGATATGATTGAAGGAATCGGTATGACHTTGTGGAAATCCAGATACAAAC      | 1016 |
| DB | 1086 | GCCATTTAGAGATATGATAGAAGGAATCGGATGGATCTGAAGAAATCGAGATACAAGAA      | 1145 |
| QY | 1017 | TTTTCGATGAGCTATATCTCTATTGTTTACTATGTTGCTGGTACTGTAGGATTGATGAGTGT   | 1076 |
| DB | 1146 | TTTCGATGAGCTGTATCTTTACTGTATATTGTGGCTGGTACAGTTGGCTTTGATGAGTGT     | 1205 |
| QY | 1077 | TCCAGTTATGGGTTATGCACTTGAATCAAAGGCAACACAGAGAGTGTATATAATGCTGC      | 1136 |
| DB | 1206 | ACCAGTAATGGGCATGTGCACCTGANTCTTAGGCAACACAGAAAGTGTGTATATGACG       | 1265 |
| QY | 1137 | TTTGGCTTTAGGCGTTGCAAACTAACTAACCAATATACTCAGAGATGTGAGAGAAGATGC     | 1196 |

|  |   |  |      |
|--|---|--|------|
| Db   | 1398  | TGAGGACATTTTTCGTGGAAAAAGTTACACACAAATCGAGGATTTTATGAGAGCAAAAT    | 143  |
| QY   | 1314  | TCAGAGGGCGAGGAAATTCCTTTGATGAGTCACAGAGAAAGTGTCACAGAACTCGACTCTGC | 137  |
| Db   | 1458  | CAAAAGGGCTAGAAAATCTATGATGATGCAGAAAAGAGTCCCCCGAACTCAGCTCCGC     | 151  |
| QY   | 1374  | TAGTAGATGCCCTGTGTTAACACGCGTCTGTTGTATCGCAAGATATTGGACGAGATTGA    | 143  |
| Db   | 1518  | GAGCAGATTGCCCTGTGTGGCAGCGTTGCTTTTATAGAAAAATATTGGATGACATAGA     | 157  |
| QY   | 1434  | AGCCACGACTACACAACACTTCACIAGGAGGCGCTATGTTAGCAAGCCAAAGAACTTCT    | 149  |
| Db   | 1578  | AGCAATGACTACACAATTTTCACAAAAGGGCTTATGTATAACAGGCAAGCAAGAGCTATT   | 163  |
| QY   | 1494  | CACCTTGGCCATTGCTTATGCAAAATCTCT                                 | 1523 |
| Db   | 1638  | AGTATGCCGTAGCATGTGCCAAGTCTCT                                   | 1667 |
| RESULT 12  |   |  |      |
| ID   | AAV16948  |  |      |
| XX   | AAV16948 standard; cDNA to mRNA; 2085 BP.                               |  |      |
| XX   | AAV16948;   |  |      |
| DT   | 06-JUL-1998 (first entry)   |  |      |
| DE   | Nucleic acid encoding phytoene synthase 1.                              |  |      |
| XX   | Phytoene synthase; breeding; variable flower colour; ds.                |  |      |
| KW   | Gentiana lutea.   |  |      |
| OS   |   |  |      |
| FH   | Key   | Location/Qualifiers  |      |
| FT   | CDS   | 586..1866  |      |
| FT   |   | /*tag= a   |      |
| XX   |   |  |      |
| PN   | JP10084966-A.   |  |      |
| PD   | 07-APR-1998.  |  |      |
| XX   |   |  |      |
| PF   | 17-SEP-1996; 96JP-0245107.  |  |      |
| XX   |   |  |      |
| PR   | 17-SEP-1996; 96JP-0245107.  |  |      |
| XX   |   |  |      |
| PA   | (IWAT-) IWATE KEN.  |  |      |
| XX   |   |  |      |
| DR   | WPI; 1998-264853/24.  |  |      |
| DR   | P-PSDB; AAW46961.   |  |      |
| XX   |   |  |      |
| PT   | Phytoene synthase gene - useful for breeding plant of variable          |  |      |
| PT   | flower colour   |  |      |
| XX   |   |  |      |
| PS   | Claim 1; Pages 5-7; 15pp; Japanese.                                     |  |      |
| CC   | The present sequence encodes phytoene synthase 1. It was isolated from  |  |      |
| CC   | a cDNA library prepared from mRNA extracted from the petals of Gentiana |  |      |
| CC   | lutea. The nucleic acid sequence was amplified from the library using   |  |      |
| CC   | PCR primers AAV16952-53. The phytoene synthase gene is useful for       |  |      |
| CC   | breeding plants with variable flower colours.                           |  |      |
| XX   |   |  |      |
| SQ   | Sequence 2085 BP; 654 A; 320 C; 479 G; 632 T; 0 other;                  |  |      |
| Query Match 38.8%; Score 670.4; DB 19; Length 2085;          |   |  |      |
| Best Local Similarity 72.0%; Pred. No. 9.8e-181;             |   |  |      |
| Matches 929; Conservative 0; Mismatches 331; Indels 30; Gaps |   |  |      |
| QY   | 240   | TTTCATGAGCATGCTGTGCTTGTGTTGGTGTGTTCTCCACATTCGAGGCTCGAA         | 299  |
| Db   | 576   | TTCTGTTACATGCTCTATTGTGACGATGCGGTGTTTCCCGAGTCTCTGAAGTTTGAG      | 635  |
| QY   | 300   | TGGACAGGATTTGGATTTCAGTCCGAGAAGAAACCGCGTCTTTGTATCATCAGGTT       | 359  |

Db 636 TGCAATGTTTCTTGTGGAGCAATTCGAGAAAGTTACCAATTTTCG----- 681  
QY 360 CCTAGCTCGAGATAGGAAATTTGATGTGGAATCGAGAAATCAAGAAAGTGGGAGACAAAG 419  
Db 682 -----GATAAAGTTTAAATGTACAAATGAAGAGTTAAGAAAGTAGACACCAAG 731  
QY 420 GTGGAATTTTGGCTCTTAAATGCTGATCCAAAGATATTCATGCTTGGGTGGATCAAGAAC 479  
Db 732 GCGTAGATCAGTTTNGGGGTTGGAGATTGAGTTTCATTTGCTTGAGAGAGTCTGGATT 791  
QY 480 TGAAG-----AGGGAAGCAGTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCAGCTGGAGA 536  
Db 792 AGAGACCCCGGAAGAAGATTATCGGCTATCCTCCATATTTATAGCTAAACCCCGSCAGAG 851  
QY 537 AATGACTGTCTATCAGAGAAAAGGTGATGATGTGGTATTAAAGCAGGACGCTTTAGT 596  
Db 852 AATAGACATGACATCAGAGCAAAAGTTTATGATGTCGTTTAAAGCAAGCAGCTTTGAT 911  
QY 597 GAAGAGCAGCTGAGATCTACCGATGATTTAGAAGTGAAGCCGATATTTGCTTTCAGG 656  
Db 912 TATAGACATTGAGGTCTAGAGAAATTTGGAGGTGAACCCGACATATTTTGGCAGG 971  
QY 657 GAATTTGGCTTGTGAGTGAAGCATATGATCTGTGGCAAGTATGTGCAGAGTATGC 716  
Db 972 AAACGCAACGTTGTAATGAAGCTATGATCGGTGTCGAGAGATATGTGCTGAATATGC 1031  
QY 717 AAGACATTTTACTTAGAACCAAGCTATGACCCAGAGAGAAAGAGCTATCTGGGC 776  
Db 1032 CAAGTCATTTACTTGGGGAACCCAGCTCATGACCCGAGAGCGTTTAGCTATCTGGGC 1091  
QY 777 ---AATATATGTGTGTCAGGAGAACGGATGAGCTGTGTGATGGCCCTAATCATCCCA 833  
Db 1092 CGATATATATGATGCGGTAGGAGGACAGATGAGCTGTGTGATGGCCCTAATCATCCCA 1151  
QY 834 CATAACTCCCAAGCTTTAGATAGTGGGAGACAGCTGGAAGATATTTTCACTGGGCG 893  
Db 1152 CATAAATCCACCCGCTTAGATAGTGGGAGCAAGATCAGAGATGTTTTCACAGGCA 1211  
QY 894 GCATTTGATATGCTGTGATGCTCTTTATCCGATATGCTCCAGATTTTCTGTTGAT 953  
Db 1212 ACCTCTGGATGATGCTGTGCTCTTTATCTGATACCATTTACCAAGTATCCTGTGGACAT 1271  
QY 954 TCAGCCATTCAGAGATGATGATCAAGGAATCGCTATGGACTTCTGGAATCCAGATACAA 1013  
Db 1272 CCAGCCATTTAGAGATGATGATAAGGAATGCGGATGGATCTGAAGAAATCGAGATACAA 1331  
QY 1014 AACTTTGATGAGCTATATCTCTATTGTTACTATGTTGCTGTGCTAGGATTTGATGAG 1073  
Db 1332 GAATTTGATGAGCTGATCTTTACTGCTATTATGTTGGTGGCAGACAGTTGGCTTTGATGAG 1391  
QY 1074 TGTTCAGTTATGGGTATTCGACCTGAATCAAAAGGCAACACAGAGAGTGTATATATGC 1133  
Db 1392 TGTACCAAGTAAATGGGATTTGCACCTGAATCTAAGGCAACACAGAAAGTGTGTATGATGC 1451  
QY 1134 TGTTTTGGCTTTAGGCTTCCAAATCAACTAATCACTACTCAGAGATGTAGAGAAAGA 1193  
Db 1452 AGCTTATCTTTGGGATCGCAACAGCTGACTACATTTCTAAGGGATTTGGAGAAAGA 1511  
QY 1194 TGCAGAGAGGAGAGTATCTTGGCTCAAGATGAATTAGCAGACAGCGGCTCTCCGA 1253  
Db 1512 TCGAAGAGAGGAGAGTGTACCTACCTCAAGATGAATTAGCAGACAGCGGTTTATCAGA 1571  
QY 1254 CGAAGACATATTTGCTGGAAGAGTGTACTGATAGTGGAGAACTTTATGAAGAAACAAAT 1313  
Db 1572 TGAGGACATTTTGTCTGGGAAAGTTACAGACAAATGGAGATTATTTATGAAGAAACAAAT 1631  
QY 1314 TCAGAGGCGGAGGAAATTTCTTATCAGTCAGAGAAAGTGTCCAGAACTTGCAGCTGCG 1373  
Db 1632 CAAAGGGCTAGAAAATTTCTNATGATGTCAGAGAAAGGAGTCCCCGAACTCAGCTCCCG 1691  
QY 1374 TAGTAGATGCCCTGTGTAAACAGCGCTGTGTGTATCGCAAGATATTTGGACGAGATTGA 1433  
Db 1692 GAGCAGATTCCCTGTGTGGGCAACCGTTGCTTTTTTATGAAAATATTTGGATGAGATAGA 1751

QY 1434 AGCCAGGACTACAACTTCACAGGAGGGCTTATGTAGCAAGCCAAAGAGCTTCT 1493  
Db 1752 AGCAATGTAGCTACAACTTCACAGGAGGGCTTATGTAGCAAGCCAAAGAGCTTCT 1811  
QY 1494 CAGCTTGGCCCATGCTTATGCAAAATCTCT 1523  
Db 1812 AGCTATGCTGTAGCATGTGCCAAGTCTCT 1841

## RESULT 13

AAV16950  
ID AAV16950 standard; cDNA to mRNA; 1932 BP.

XX AAV16950;

DF 06-JUL-1998 (first entry)

XX Nucleic acid encoding phytoene synthase 3.

KW Phytoene synthase; breeding; variable flower colour; ds.

XX Gentiana lutea.

XX Key Location/Qualifiers  
CDS 499..1785  
/\*tag= a

PN JP10084966-A.

PD 07-APR-1998.

PF 17-SEP-1996; 96JP-0245107.

PR 17-SEP-1996; 96JP-0245107.

XX (IWAT-) IWATE KEN.

XX WPI; 1998-264853/24.

DR P-PSDB; AAW46963.

PT Phytoene synthase gene - useful for breeding plant of variable flower colour

PS Claim 3; Pages 10-12; 15pp; Japanese.

XX The present sequence encodes phytoene synthase 3. It was isolated from a cDNA library prepared from mRNA extracted from the petals of *Gentiana lutea*. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-53. The phytoene synthase gene is useful for breeding plants with variable flower colours.

XX Sequence 1932 BP; 635 A; 302 C; 434 G; 561 T; 0 other;

Query Match 37.8%; Score 653.4; DB 19; Length 1932;  
Best Local Similarity 72.6%; Pred. No. 6.8e-176;  
Matches 940; Conservative 0; Mismatches 321; Indels 34; Gaps 6;

QY 240 TTTTCATGAGCATCTGTTGCTTTGTTGCTGTTGTTTCTCCCACTTCCGAGGCTCGAA 299

Db 489 TTTCTTACATGCTCTATTGTAGCTATGGTTGTTTCCCGAGTCTGAAGTTTGAG 548

QY 300 TGGACAGGATTTGGATTCAGTCCGAGAAAGAAACCGGCTCTTTGTATCATCCAGTT 359

Db 549 TGCAATGTTTCTTGGAGCAATTCGAGAAAGTTACCATTTTCG----- 594

QY 360 CCTAGCTCGAGATAGGAATTTGATGGAGATCAAGAAAGTGGGAGACAAAG 419

Db 595 -----GATAAAGTTTAAATGTACAATGGAAGAGTTAAGAAAAATGACACCAAG 644

QY 420 GTGGAATTTTGGCTCTTTAATTCGTATCCCAAGATATTTCATGCTTGGTGGATCAAGAC 479

Db 645 GCGTAGATCAGTTATGGGCTTGAGATTTCAGTTTCATTTGCTTGAGAGTCTGGATT 704

QY 480 TGA---AGGAAACACCTTCTGTACAGTCCAGTCTGGCTAGCCAGCTGGAGA 536  
Db 705 AGAGACCCCGGAAGAGATATCGTATCCCTCCAGTATATAGCTACCCCGCAGGAGA 764  
QY 537 ATGACTGTGTCATCAGAGAAAGAGTGTATGATGTGTATTAAGCAGGAGCTTTAGT 596  
Db 765 AATGACGATGATCAGAGCAAGAGTTTATGATGCTGTTTAAAGCAGCAGCTTTGAT 824  
QY 597 GAAGAGGAGCTGAGATCTACCGATGATTAGAACTGAAGCCGATATTTGTTTCCAGG 656  
Db 825 TAATAGACAGTTGAGCTAGAGAAATTTGAGGTGAACCGACATATTTTCCAGG 884  
QY 657 GAATTTGGCTTTGAGTGAAGCATATGATCGTTGGCCGAAGTATGTGCAGATATGC 716  
Db 885 AAACGCAACGCTTTGAATGAAGCTTATGATCGGTGTGAGAAATGTGTGCTGAATATGC 944  
QY 717 AAAGACATTTTACTTGAAGCAACCAAGCTAATGACCCACAGAGCAAGAGCTATCTGGC 776  
Db 945 CAAGTCATCTACTGGGAACCCAGCTCATGACCCGAGAGGCGTTTAGCTATCTGGGC 1004  
QY 777 AATATATGTGTGTGAGGAGAACGATGAGCTTGTGATGGCCCTAATGATCCACAT 836  
Db 1005 GATATATGTGTGTGAGGAGACAGATGAGCTTGTGATGGCTTAAGCGCTCACAAT 1064  
QY 837 AACTCGCAAGCTTTAGATAGTGGGAGACAGGCTGGAAGATATTTCAAGTGGCGGCC 896  
Db 1065 AATCCCAACCGGTTAGATAGTGGGAAGCAAGATTAGAAGATGTTTCAAGGGCAACC 1124  
QY 897 ATTTGATATGCTGTGCTGCTTTATCCGATACTCTCCAGATTTCCCTGTTGATATCA 956  
Db 1125 TTTTGATATGCTGTGCTGCTTTATCTGATACCATTAACCAAGTATCTGTGGACATCCA 1184  
QY 957 GCCATTGAGATATGATTGAAGGAATGCTATGACCTGTGGAATCCAGATACAAAC 1016  
Db 1185 GCCATTGAGATATGATAGAGGAATGCGGATGATCTGAAGAATCGAGATACAGAA 1244  
QY 1017 TTTGATGAGCTATATCTCTATGTTACTATGTTCTGGTACTGTAGGATGATGAGTGT 1076  
Db 1245 TTTGATGAGCTATATCTCTATGTTACTATGTTCTGGTACTGTAGGATGATGAGTGT 1304  
QY 1077 TCCAGTATGCTGTTGACCTGATCAAGGCAACAGCAGATGATATTAATGCTGC 1136  
Db 1305 ACCAGTATGCTGTTGACCTGATCAAGGCAACAGCAGATGATATTAATGCTGC 1364  
QY 1137 TTTGCTTTAGGCTTGAACATCAACTAACCAATATCTCAGAGATGTAGGAGAGATGC 1196  
Db 1365 TTTATCTTTGGGATCGGGAACCACTGACTAACAATCTAAGGATGTGGAGAGATGC 1424  
QY 1197 CAGAGAGAGAGATATCTTCCCTCAGATGAATAGCAGGAGGCTCTCCGACGA 1256  
Db 1425 AAGAGAGGAGAGTGTACCTACCTCAAGATGAATAGCAGGAGGTTTATCAGATGA 1484  
QY 1257 AGACATATTTGCTGGAAGAGTCACTGATAGTGAAGGAACTTTATGAAGAACTTCA 1316  
Db 1485 GGCATTTTGTGGAAGTTCAGACAAATGGAAGATTTTATGAAGAGCAATCA 1544  
QY 1317 GAGGCGAGGAAATCTTTGATGA-GTCAGAGAAAGGTGTACAGAACTGGACTCTG-CT 1374  
Db 1545 AAGGCTAGAAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1604  
QY 1375 AGTAGAGGCTGTGT----TAACAGCGCTGCTGTTGATGCCAAGATATTTGACGAGAT 1430  
Db 1605 AGCAGATGCTGTGTGGGCGAGCGCTTTGCTTTTATAGGAAATATTTGATGATGAT 1664  
QY 1431 TGAAGCCACGACTACACAACTTC-ACAAGGAGGCTTATGTTAGCAAGCCAAAGAC 1489  
Db 1665 AAGAGCAATGACTACAACTTTCAACAAAAGGCTTATGTTAAACAGGCAAGAGAC 1724  
QY 1490 TTTCACTCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 1524  
Db 1725 TATTAGCTATGCTGTAGCATGTGCAAGTCTCTT 1759

## RESULT 14

AAC35120

ID AAC35120 standard; DNA; 1703 BP.

XX AAC35120;

AC AAC35120;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 9067.

DE Arabidopsis thaliana

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
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PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0153070.
PR 10-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 33.5%; Score 578.6; DB 21; Length 1703;
Best Local Similarity 73.4%; Pred. No. 1.5e-154;
Matches 769; Conservative 0; Mismatches 269; Indels 9; Gaps 2;
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Db 475 AAGTAGAAGAAATTGGTGTCTTCAAGCTTAGTAGCAAGTCTTCTCGAGAGATAGC 534
QY 543 TGTGTCATCAGAGAAAAGGTGTATGATGTGGTATTAAACGACGACGCTTGTAGTAGAG 602
Db 535 TCTTTCATCTGAAGAGAAGGTTTACAATGTGTGTGTAAGAAAGCTGCTTTGGTGAACA 594
QY 603 GCAGCTGAG---ATCTACCATGATTTAGAAAGTGAAG-----CCGCGATATGTTGTTCC 653
Db 595 ACAGCTAAGGTCTTCTTCTTATGATTTGATGTGAAGAAACACAGATGTTGTTCTTCC 654
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PR 24-JUN-1999; 99US-0140695.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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PR 13-JUL-1999; 99US-0143542.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
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PR 19-JUL-1999; 99US-0144332.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 13-AUG-1999; 99US-0148565.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.

PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 33.5%; Score 578.4; DB 21; Length 1566;
Best Local Similarity 72.5%; Pred. No. 16e-154;
Matches 766; Conservative 0; Mismatches 281; Indels 9; Gaps 1;

QY 474 AGAACTGAAAGGGAAGCAGCTTTCTCTGTACAGTCCAGTTTGTGTGCTAGCCAGCTGG 533
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Db 329 AAGGAACCGAAGTAGAAGAAATTTGGTGTGCTTCAAGCTTAGTAGCAAGCTCTCTGG 388
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QY 534 AGAAATGACGTGTCTCATCAGAGAAAGGTCTATGTATGCTGTATTAAGCAGGAGCTTT 593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AGAGATAGCTCTTTCATCTTGAAGAGGTTTACAATGTTGTGTGTAACCAAGCTGCTTT 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 594 AGTGAAGAGGAGCTGAGATCTAC-----CGATGATTTAGAAGTGAAGCCGGATAT 644
    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 449 GGTGAACAACACGCTAAGGTCTTCTTTATGACCTTGATGTGAAGAACCACAGATGT 508
    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 645 TGTGTTCCAGGGAATTTGGCTTTGTGTGAGTGAAGCATATGATCGTTGTGCGCAAGTATG 704
    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 509 TGTCTCTCTGGGAGTTTGTGTTGGTGAAGCTTATGATCGATCGCGTGAAGTTTG 568
    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 705 TGCAGACTATGCAAGACATTTTACTTAGGNACCAAGCTATGACCCAGAGAGAGAG 764
    || || || || || || || || || || || || || || || || || || || || ||
Db 569 CGCTGAATATGCTAAGACGTTTATCTTGGAACTTTGTTATGACCCGAAAGCGGAAA 628
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QY 765 AGCTATCTGGCAATATATGTGTGTGTCAGGAGAACGATGAGCTTGTGTGATGCCCTAA 824
    || || || || || || || || || || || || || || || || || || || || ||
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